

Serial Number: 097852, 922

CRF Processing Date: _____
 Edited by: _____
 Verified by: _____ (STIC sta

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED** #2
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning end of files; ☐ secretary initials/filename at end of file.
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,922

DATE: 06/21/2001

TIME: 10:22:29

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\06202001\I852922.raw

2 <110> APPLICANT: TOYO BOSEKI KABUSHIKI KAISHA
 4 <120> TITLE OF INVENTION: MODIFIED THERMOSTABLE DNA POLYMERASE
 6 <130> FILE REFERENCE: 000053
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/852,922
 C--> 9 <141> CURRENT FILING DATE: 2001-05-10
 11 <150> PRIOR APPLICATION NUMBER: 2000-138796
 12 <151> PRIOR FILING DATE: 2000-05-11
 14 <160> NUMBER OF SEQ ID NOS: 28
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 5342
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Pyrococcus kodakaraensis
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (156)..(5165)
 26 <223> OTHER INFORMATION: 1374-2453 intron, 2709-4316 intron
 28 <400> SEQUENCE: 1
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 33 cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac 173
 34 Met Ile Leu Asp Thr Asp
 35 1 5
 37 tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221
 38 Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu
 39 10 15 20
 41 aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269
 42 Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe
 43 25 30 35
 45 tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317
 46 Tyr Ala Leu Leu Lys Asp Ser Ala Ile Glu Glu Val Lys Lys Ile
 47 40 45 50
 49 acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365
 50 Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys
 51 55 60 65 70
 53 gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413
 54 Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr
 55 75 80 85
 57 ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461
 58 Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu
 59 90 95 100
 61 cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag 509
 62 His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys
 63 105 110 115
 65 cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag 557
 66 Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu
 67 120 125 130

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70 Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu
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73 gag ttc gcc gag ggg cca atc ctt atg ata agc tac gcc gac gag gaa      653
74 Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu
75                               155                               160                               165
77 ggg gcc agg gtg ata act tgg aag aac gtg gat ctc ccc tac gtt gac      701
78 Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp
79                               170                               175                               180
81 gtc gtc tcg acg gag agg gag atg ata aag cgc ttc ctc cgt gtt gtg      749
82 Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val
83                               185                               190                               195
85 aag gag aaa gac ccg gac gtt ctc ata acc tac aac ggc gac aac ttc      797
86 Lys Glu Lys Asp Pro Asp Val Leu Ile Thr Tyr Asn Gly Asp Asn Phe
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90 Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu Lys Leu Gly Ile Asn Phe
91 215                               220                               225                               230
93 gcc ctc gga agg gat gga agc gag ccg aag att cag agg atg ggc gac      893
94 Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys Ile Gln Arg Met Gly Asp
95                               235                               240                               245
97 agg ttt gcc gtc gaa gtg aag gga cgg ata cac ttc gat ctc tat cct      941
98 Arg Phe Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr Pro
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102 Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val
103                               265                               270                               275
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106 Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu Lys Val Tyr Ala Glu Glu
107                               280                               285                               290
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110 Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn Leu Glu Arg Val Ala Arg
111 295                               300                               305                               310
113 tac tcg atg gaa gat gcg aag gtc aca tac gag ctt ggg aag gag ttc      1133
114 Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr Glu Leu Gly Lys Glu Phe
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117 ctt ccg atg gag gcc cag ctt tct cgc tta atc ggc cag tcc ctc tgg      1181
118 Leu Pro Met Glu Ala Gln Leu Ser Arg Leu Ile Gly Gln Ser Leu Trp
119                               330                               335                               340
121 gac gtc tcc cgc tcc agc act ggc aac ctc gtt gag tgg ttc ctc ctc      1229
122 Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu
123                               345                               350                               355
125 agg aag gcc tat gag agg aat gag ctg gcc ccg aac aag ccc gat gaa      1277
126 Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Asp Glu
127                               360                               365                               370
129 aag gag ctg gcc aga aga cgg cag agc tat gaa gga ggc tat gta aaa      1325
130 Lys Glu Leu Ala Arg Arg Arg Gln Ser Tyr Glu Gly Gly Tyr Val Lys
131 375                               380                               385                               390
133 gag ccc gag aga ggg ttg tgg gag aac ata gtg tac cta gat ttt aga      1373

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138	Cys	His	Pro	Ala	Asp	Thr	Lys	Val	Val	Val	Lys	Gly	Lys	Gly	Ile	Ile	
139				410					415					420			
141	aac	atc	agc	gag	gtt	cag	gaa	ggt	gac	tat	gtc	ctt	ggg	att	gac	ggc	1469
142	Asn	Ile	Ser	Glu	Val	Gln	Glu	Gly	Asp	Tyr	Val	Leu	Gly	Ile	Asp	Gly	
143				425				430					435				
145	tgg	cag	aga	gtt	aga	aaa	gta	tgg	gaa	tac	gac	tac	aaa	ggg	gag	ctt	1517
146	Trp	Gln	Arg	Val	Arg	Lys	Val	Trp	Glu	Tyr	Asp	Tyr	Lys	Gly	Glu	Leu	
147		440					445					450					
149	gta	aac	ata	aac	ggg	tta	aag	tgt	acg	ccc	aat	cat	aag	ctt	ccc	gtt	1565
150	Val	Asn	Ile	Asn	Gly	Leu	Lys	Cys	Thr	Pro	Asn	His	Lys	Leu	Pro	Val	
151	455				460				465						470		
153	gtt	aca	aag	aac	gaa	cga	caa	acg	aga	ata	aga	gac	agt	ctt	gct	aag	1613
154	Val	Thr	Lys	Asn	Glu	Arg	Gln	Thr	Arg	Ile	Arg	Asp	Ser	Leu	Ala	Lys	
155				475				480						485			
157	tct	ttc	ctt	act	aaa	aaa	gtt	aag	ggc	aag	ata	ata	acc	act	ccc	ctt	1661
158	Ser	Phe	Leu	Thr	Lys	Lys	Val	Lys	Gly	Lys	Ile	Ile	Thr	Thr	Pro	Leu	
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161	ttc	tat	gaa	ata	ggc	aga	gcg	aca	agt	gag	aat	att	cca	gaa	gaa	gag	1709
162	Phe	Tyr	Glu	Ile	Gly	Arg	Ala	Thr	Ser	Glu	Asn	Ile	Pro	Glu	Glu	Glu	
163			505				510					515					
165	gtt	ctc	aag	gga	gag	ctc	gct	ggc	ata	cta	ttg	gct	gaa	gga	acg	ctc	1757
166	Val	Leu	Lys	Gly	Glu	Leu	Ala	Gly	Ile	Leu	Leu	Ala	Glu	Gly	Thr	Leu	
167		520					525					530					
169	ttg	agg	aaa	gac	gtt	gaa	tac	ttt	gat	tca	tcc	cgc	aaa	aaa	cgg	agg	1805
170	Leu	Arg	Lys	Asp	Val	Glu	Tyr	Phe	Asp	Ser	Ser	Arg	Lys	Lys	Arg	Arg	
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173	att	tca	cac	cag	tat	cgt	gtt	gag	ata	acc	att	ggg	aaa	gac	gag	gag	1853
174	Ile	Ser	His	Gln	Tyr	Arg	Val	Glu	Ile	Thr	Ile	Gly	Lys	Asp	Glu	Glu	
175				555				560						565			
177	gag	ttt	agg	gat	cgt	atc	aca	tac	att	ttt	gag	cgt	ttg	ttt	ggg	att	1901
178	Glu	Phe	Arg	Asp	Arg	Ile	Thr	Tyr	Ile	Phe	Glu	Arg	Leu	Phe	Gly	Ile	
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181	act	cca	agc	atc	tcg	gag	aag	aaa	gga	act	aac	gca	gta	aca	ctc	aaa	1949
182	Thr	Pro	Ser	Ile	Ser	Glu	Lys	Lys	Gly	Thr	Asn	Ala	Val	Thr	Leu	Lys	
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186	Val	Ala	Lys	Lys	Asn	Val	Tyr	Leu	Lys	Val	Lys	Glu	Ile	Met	Asp	Asn	
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189	ata	gag	tcc	cta	cat	gcc	ccc	tcg	gtt	ctc	agg	gga	ttc	ttc	gaa	ggc	2045
190	Ile	Glu	Ser	Leu	His	Ala	Pro	Ser	Val	Leu	Arg	Gly	Phe	Phe	Glu	Gly	
191	615				620				625						630		
193	gac	ggt	tca	gta	aac	agg	gtt	agg	agg	agt	att	gtt	gca	acc	cag	ggt	2093
194	Asp	Gly	Ser	Val	Asn	Arg	Val	Arg	Arg	Ser	Ile	Val	Ala	Thr	Gln	Gly	
195				635				640					645				
197	aca	aag	aac	gag	tgg	aag	att	aaa	ctg	gtg	tca	aaa	ctg	ctc	tcc	cag	2141
198	Thr	Lys	Asn	Glu	Trp	Lys	Ile	Lys	Leu	Val	Ser	Lys	Leu	Leu	Ser	Gln	

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203	665	670	675	2237
205 aaa gat cgg agc agg tat ata ctg gag ata act gga aag gac gga ttg				
206 Lys Asp Arg Ser Arg Tyr Ile Leu Glu Ile Thr Gly Lys Asp Gly Leu				
207	680	685	690	2285
209 ata ctg ttc caa aca ctc att gga ttc atc agt gaa aga aag aac gct				
210 Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala				
211 695	700	705	710	2333
213 ctg ctt aat aag gca ata tct cag agg gaa atg aac aac ttg gaa aac				
214 Leu Leu Asn Lys Ala Ile Ser Gln Arg Glu Met Asn Asn Leu Glu Asn				
215	715	720	725	2381
217 aat gga ttt tac agg ctc agt gaa ttc aat gtc agc acg gaa tac tat				
218 Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr				
219	730	735	740	2429
221 gag ggc aag gtc tat gac tta act ctt gaa gga act ccc tac tac ttt				
222 Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe				
223	745	750	755	2477
225 gcc aat ggc ata ttg acc cat aac tcc ctg tac ccc tca atc atc atc				
226 Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile				
227	760	765	770	2525
229 acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa				
230 Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu				
231 775	780	785	790	2573
233 tat gac gtt gcc cca cag gtc ggc cac cgc ttc tgc aag gac ttc cca				
234 Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro				
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238 Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys				
239	810	815	820	2669
241 ata aag aag aag atg aag gcc acg att gac ccg atc gag agg aag ctc				
242 Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu				
243	825	830	835	2717
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246 Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu				
247	840	845	850	2765
249 ccc gag gaa tgg ctt cca gtc ctc gag gaa ggg gag gtt cac ttc gtc				
250 Pro Glu Glu Trp Leu Pro Val Leu Glu Glu Gly Glu Val His Phe Val				
251 855	860	865	870	2813
253 agg att gga gag ctc ata gac ccg atg atg gag gaa aat gct ggg aaa				
254 Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys				
255	875	880	885	2861
257 gta aag aga gag ggc gag acg gaa gtg ctt gag gtc agt ggg ctt gaa				
258 Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu				
259	890	895	900	2909
261 gtc ccg tcc ttt aac agg aga act aac aag gcc gag ctc aag aga gta				
262 Val Pro Ser Phe Asn Arg Arg Thr Asn Lys Ala Glu Leu Lys Arg Val				
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267	920 925 930	
269	ctg aag tcg ggg agg aga ata aag ata acc tct ggc cac agc ctc ttc	3005
270	Leu Lys Ser Gly Arg Arg Ile Lys Ile Thr Ser Gly His Ser Leu Phe	
271	935 940 945 950	
273	tct gtg aga aac ggg gag ctc gtt gaa gtt acg ggc gat gaa cta aag	3053
274	Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys	
275	955 960 965	
277	cca ggt gac ctc gtt gca gtc ccg cgg aga ttg gag ctt cct gag aga	3101
278	Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg	
279	970 975 980	
281	aac cac gtg ctg aac ctc gtt gaa ctg ctc ctt gga acg cca gaa gaa	3149
282	Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu	
283	985 990 995	
285	gaa act ttg gac atc gtc atg acg atc cca gtc aag ggt aag aag aac	3197
286	Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn	
287	1000 1005 1010	
289	ttc ttt aaa ggg atg ctc agg act ttg cgc tgg att ttc gga gag gaa	3245
290	Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu	
291	1015 1020 1025 1030	
293	aag agg ccc aga acc gcg aga cgc tat ctc agg cac ctt gag gat ctg	3293
294	Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu	
295	1035 1040 1045	
297	ggc tat gtc cgg ctt aag aag atc ggc tac gaa gtc ctc gac tgg gac	3341
298	Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp	
299	1050 1055 1060	
301	tca ctt aag aac tac aga agg ctc tac gag gcg ctt gtc gag aac gtc	3389
302	Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val	
303	1065 1070 1075	
305	aga tac aac ggc aac aag agg gag tac ctc gtt gaa ttc aat tcc atc	3437
306	Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile	
307	1080 1085 1090	
309	cgg gat gca gtt ggc ata atg ccc cta aaa gag ctg aag gag tgg aag	3485
310	Arg Asp Ala Val Gly Ile Met Pro Leu Lys Glu Leu Lys Glu Trp Lys	
311	1095 1100 1105 1110	
313	atc ggc acg ctg aac ggc ttc aga atg aga aag ctc att gaa gtg gac	3533
314	Ile Gly Thr Leu Asn Gly Phe Arg Met Arg Lys Leu Ile Glu Val Asp	
315	1115 1120 1125	
317	gag tcg tta gca aag ctc ctc ggc tac tac gtg agc gag ggc tat gca	3581
318	Glu Ser Leu Ala Lys Leu Leu Gly Tyr Tyr Val Ser Glu Gly Tyr Ala	
319	1130 1135 1140	
321	aga aag cag agg aat ccc aaa aac ggc tgg agc tac agc gtg aag ctc	3629
322	Arg Lys Gln Arg Asn Pro Lys Asn Gly Trp Ser Tyr Ser Val Lys Leu	
323	1145 1150 1155	
325	tac aac gaa gac cct gaa gtg ctg gac gat atg gag aga ctc gcc agc	3677
326	Tyr Asn Glu Asp Pro Glu Val Leu Asp Asp Met Glu Arg Leu Ala Ser	
327	1160 1165 1170	
329	agg ttt ttc ggg aag gtg agg cgg ggc agg aac tac gtt gag ata ccg	3725

VERIFICATION SUMMARY

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L:8 M:270 C: Current Application Number differs, Replaced Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date